Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:45:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124873.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3124873 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124873_1.fastq.gz SRR3124873_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:45:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124873.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,144,596
Mapped reads	4,081,894 / 98.49%
Unmapped reads	62,702 / 1.51%
Mapped paired reads	4,081,894 / 98.49%
Mapped reads, first in pair	2,042,241 / 49.27%
Mapped reads, second in pair	2,039,653 / 49.21%
Mapped reads, both in pair	4,068,258 / 98.16%
Mapped reads, singletons	13,636 / 0.33%
Secondary alignments	0
Supplementary alignments	17,896 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	181,751 / 4.39%
Duplication rate	2.52%
Clipped reads	2,428,805 / 58.6%

2.2. ACGT Content

Number/percentage of A's	107,564,679 / 28.73%
Number/percentage of C's	73,875,916 / 19.73%
Number/percentage of T's	111,028,163 / 29.66%
Number/percentage of G's	81,671,237 / 21.81%
Number/percentage of N's	243,527 / 0.07%

GC Percentage	41.55%

2.3. Coverage

Mean	0.121
Standard Deviation	1.1452

2.4. Mapping Quality

Mean Mapping Quality	52.9

2.5. Insert size

Mean	58,883.65
Standard Deviation	2,289,030.08
P25/Median/P75	136 / 167 / 209

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,256,261
Insertions	58,653
Mapped reads with at least one insertion	1.4%
Deletions	149,515
Mapped reads with at least one deletion	3.58%
Homopolymer indels	46.69%

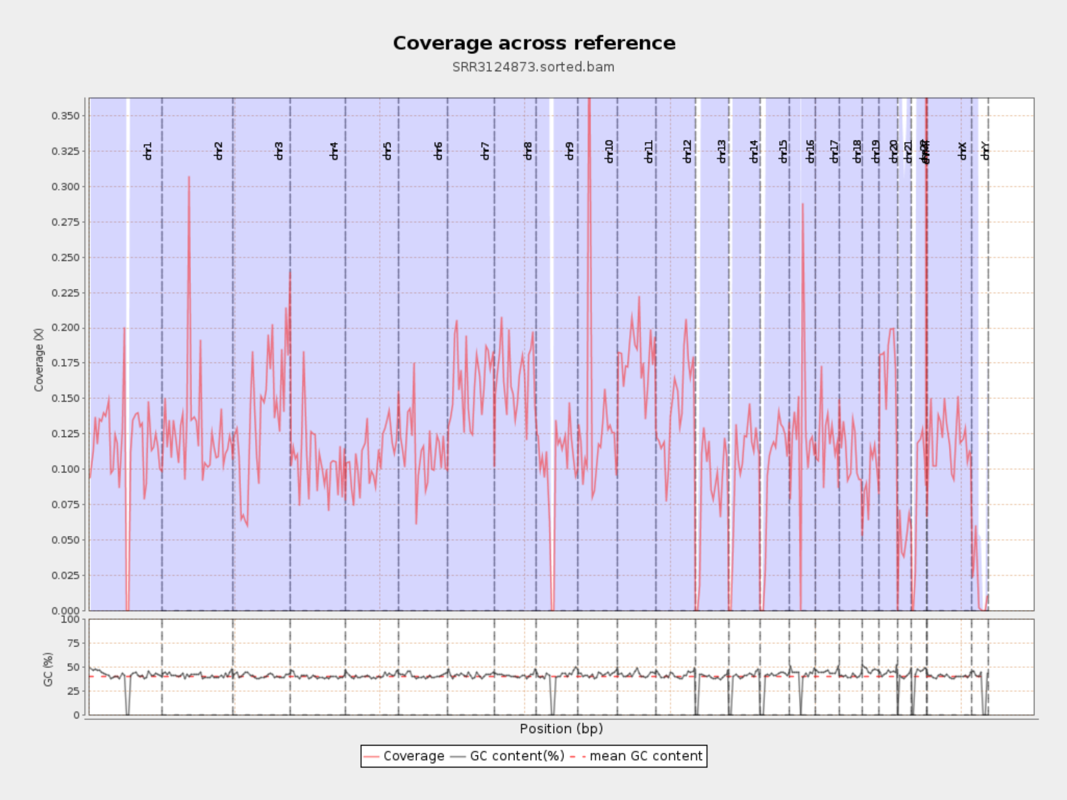
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

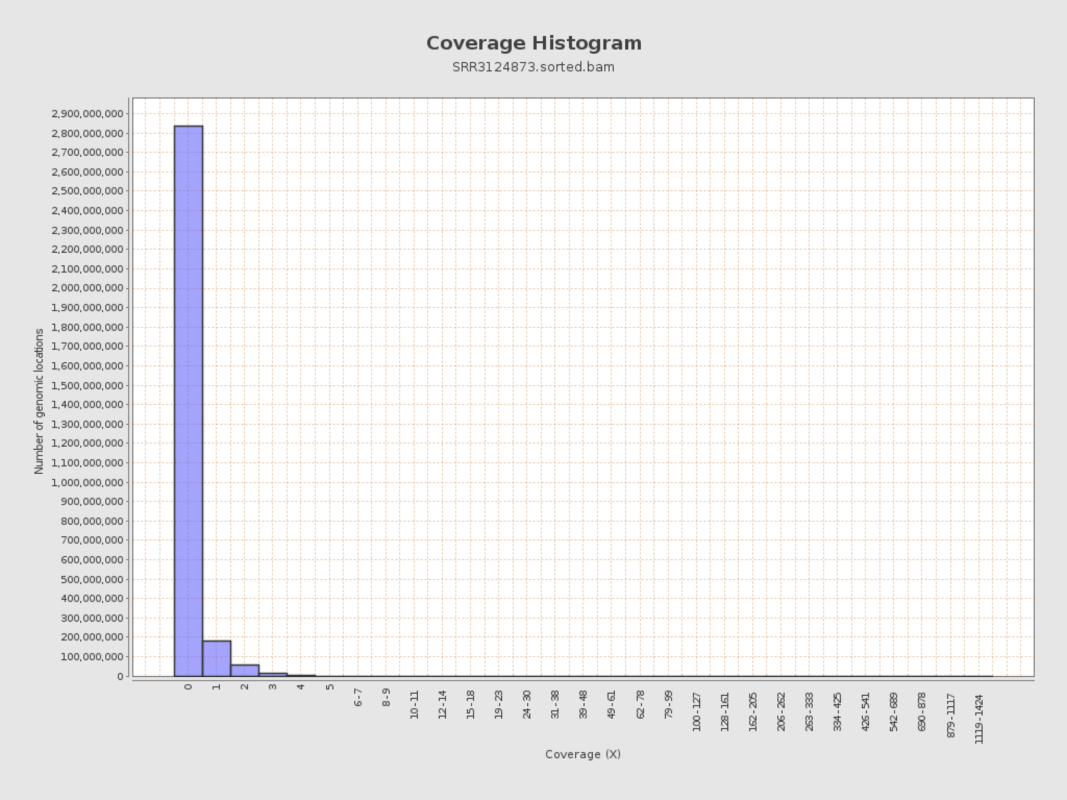
		bases	coverage	deviation
chr1	249250621	28699987	0.1151	1.1771
chr2	243199373	31058085	0.1277	1.4553
chr3	198022430	27366425	0.1382	0.514
chr4	191154276	20183787	0.1056	0.6891
chr5	180915260	19654907	0.1086	0.4308
chr6	171115067	19554076	0.1143	0.7889
chr7	159138663	25713023	0.1616	1.3623
chr8	146364022	24240992	0.1656	0.6814
chr9	141213431	14028120	0.0993	1.3331
chr10	135534747	18094178	0.1335	3.0468
chr11	135006516	24062949	0.1782	1.5683
chr12	133851895	19214861	0.1436	0.4952
chr13	115169878	9674366	0.084	0.3678
chr14	107349540	10569859	0.0985	0.439
chr15	102531392	9825354	0.0958	0.3967
chr16	90354753	11281945	0.1249	1.4178
chr17	81195210	9764755	0.1203	1.1027
chr18	78077248	8804197	0.1128	1.3926
chr19	59128983	5530440	0.0935	0.694
chr20	63025520	11183281	0.1774	0.5708
chr21	48129895	2400033	0.0499	0.3841
chr22	51304566	4059337	0.0791	0.3839
chrMT	16571	188466	11.3732	7.0521
chrX	155270560	18578535	0.1197	0.6569

chrY	59373566	925980	0.0156	0.9923

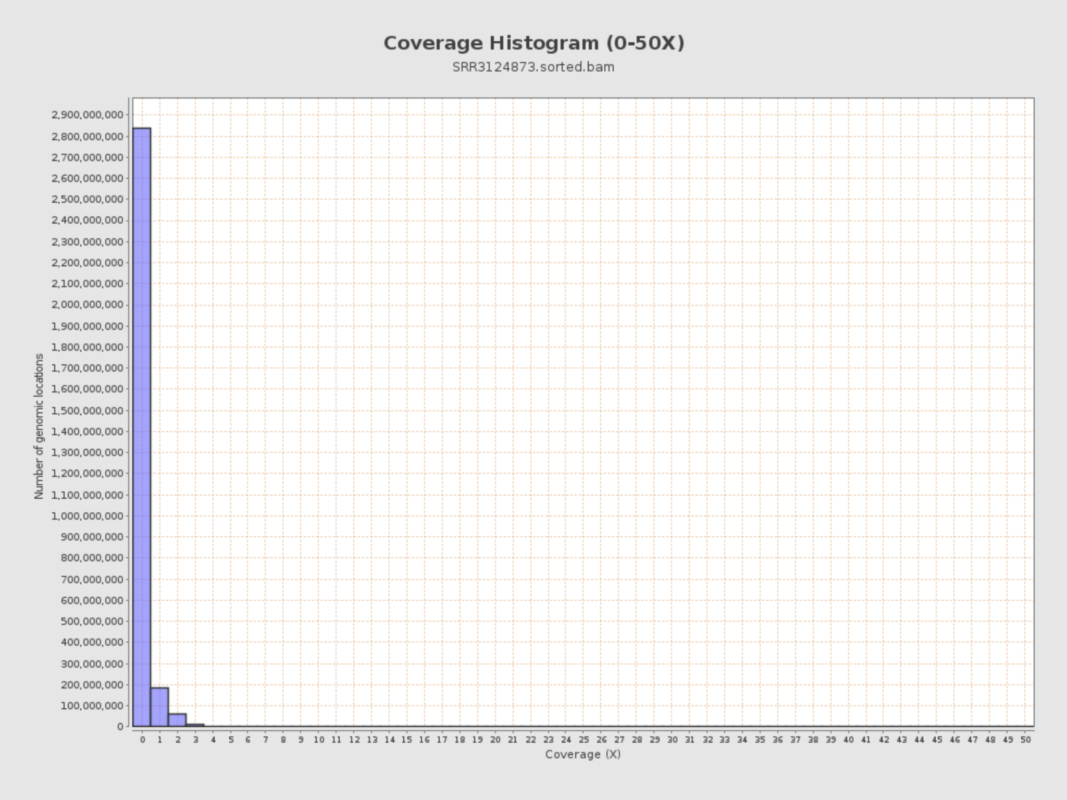
3. Results : Coverage across reference



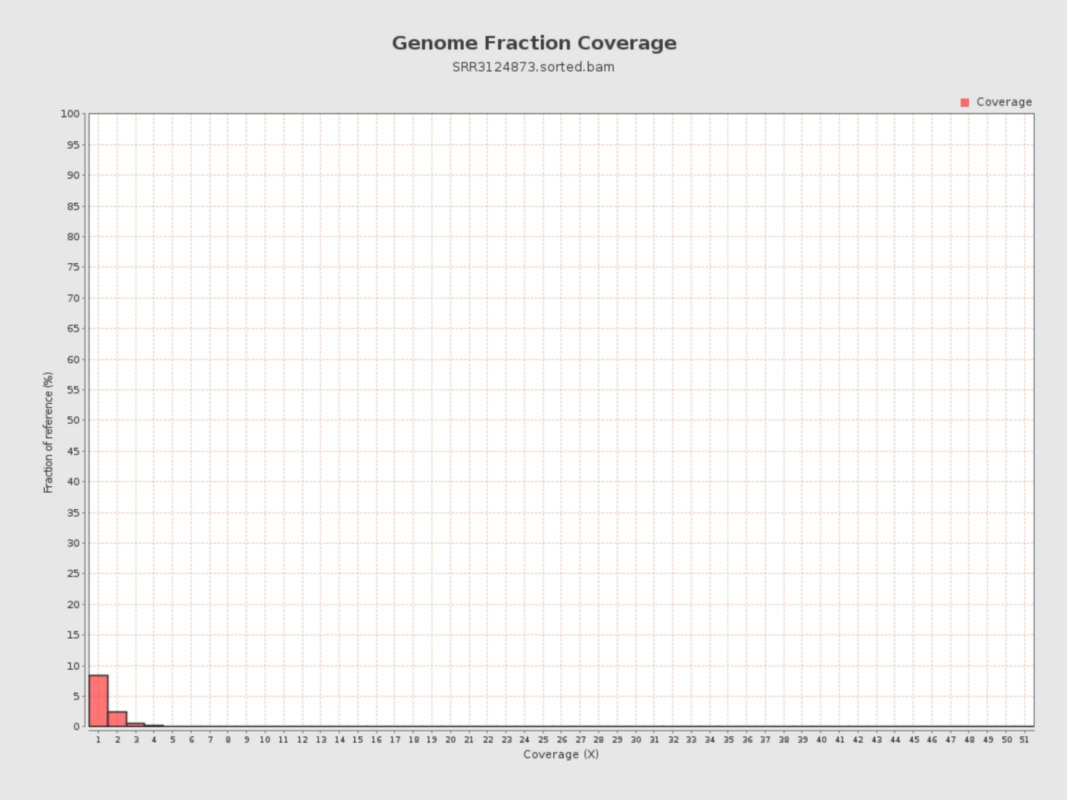
4. Results : Coverage Histogram



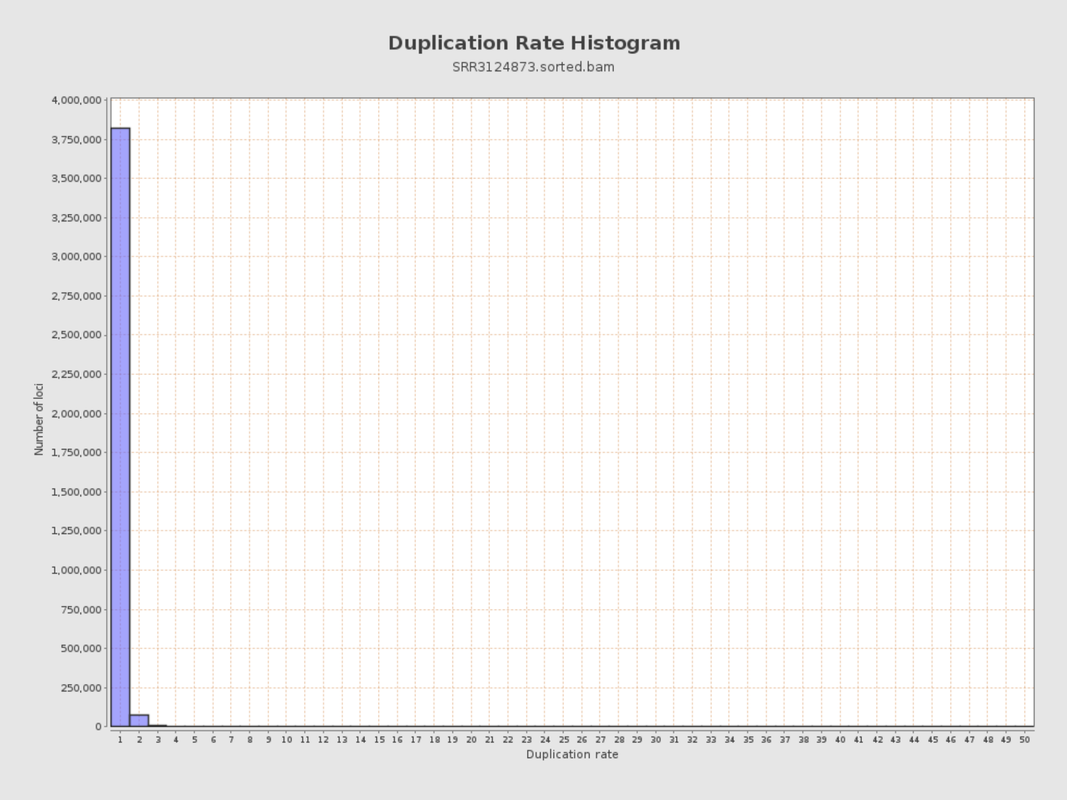
5. Results : Coverage Histogram (0-50X)



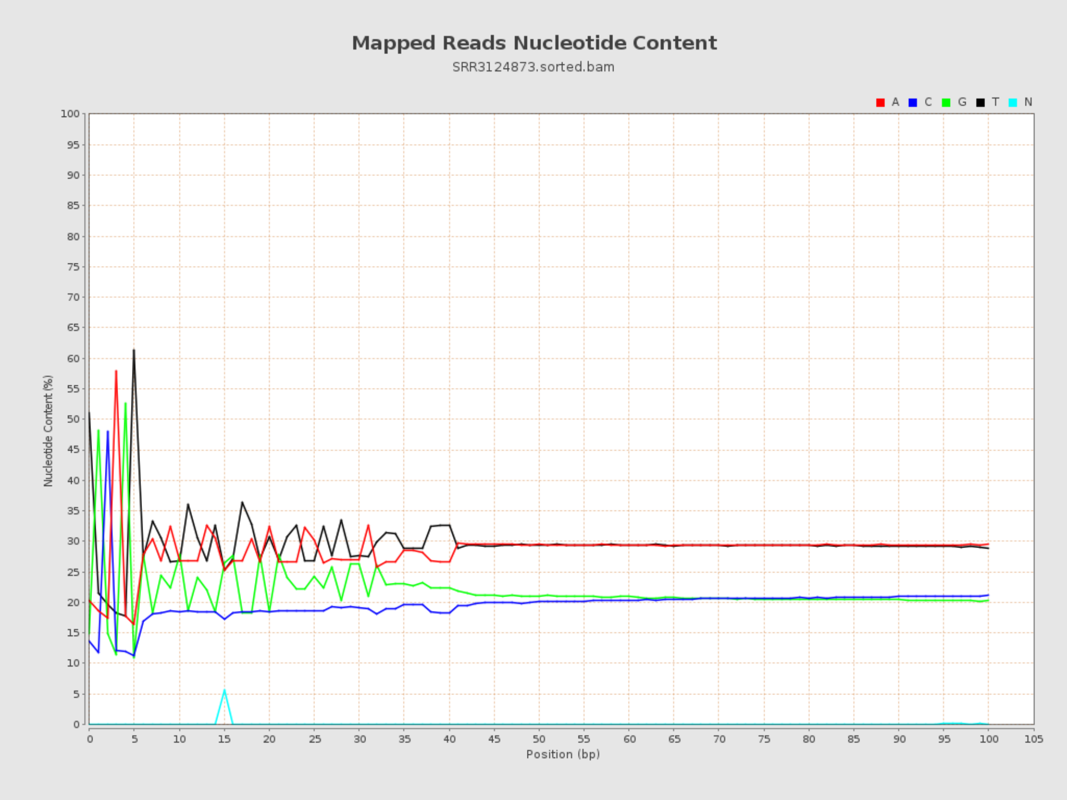
6. Results : Genome Fraction Coverage



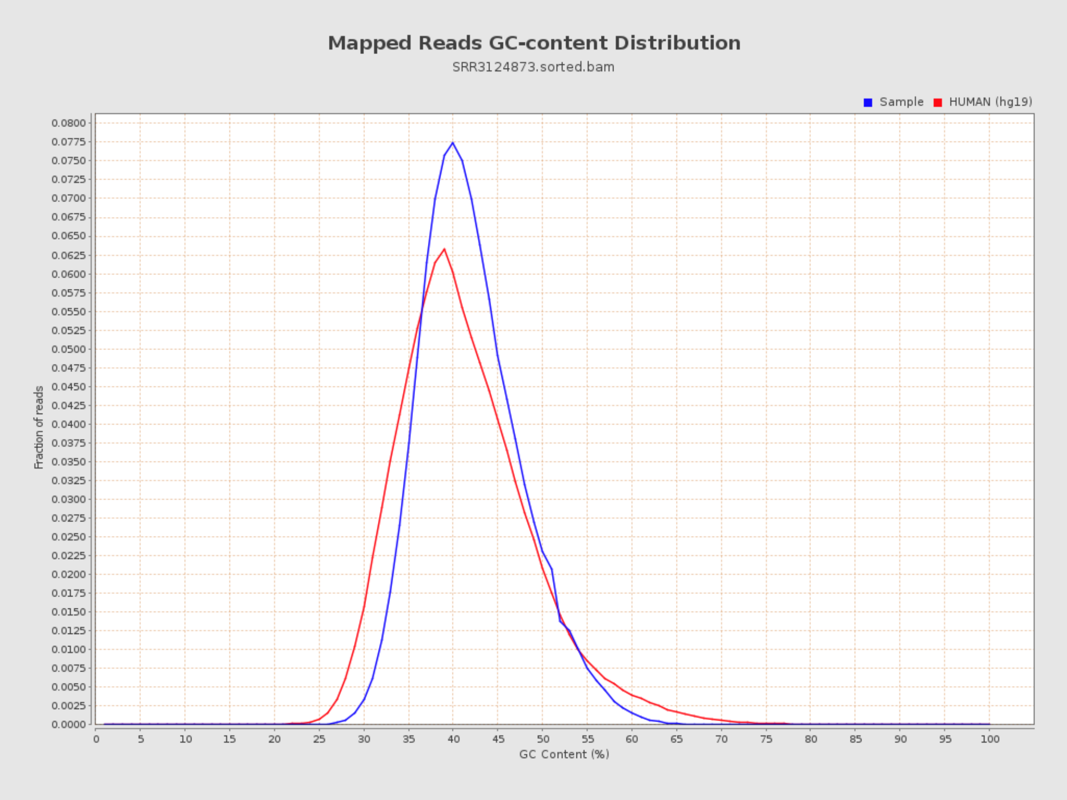
7. Results : Duplication Rate Histogram



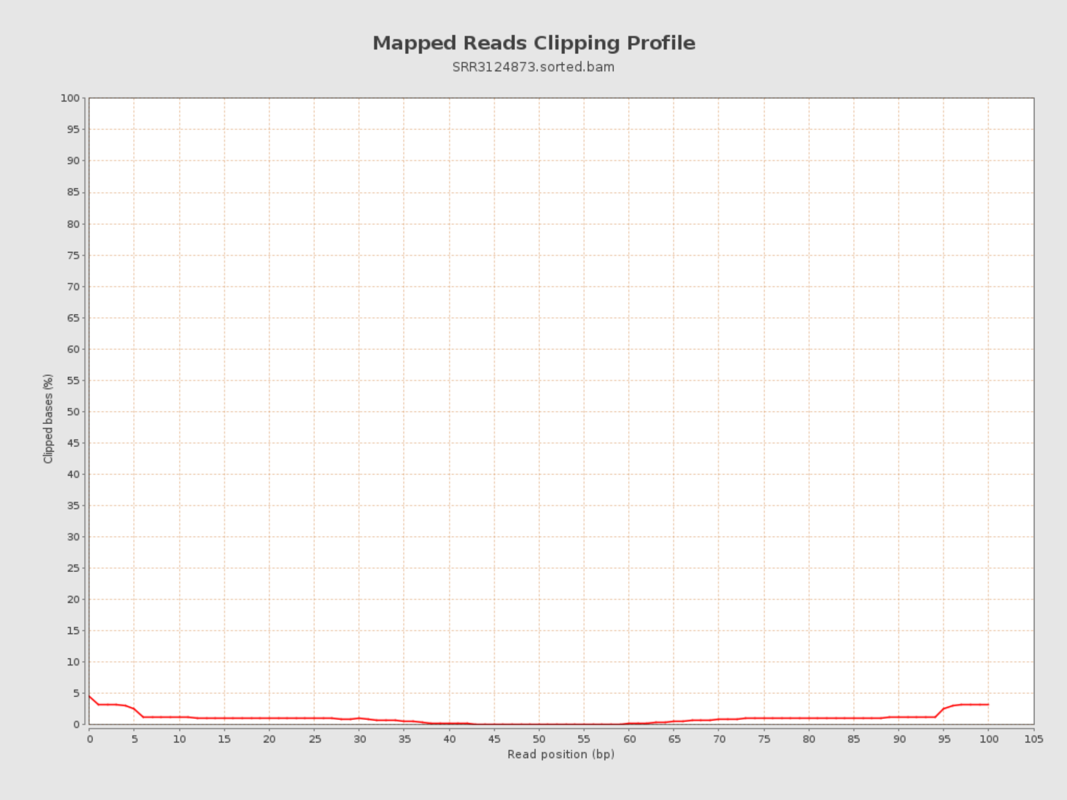
8. Results : Mapped Reads Nucleotide Content



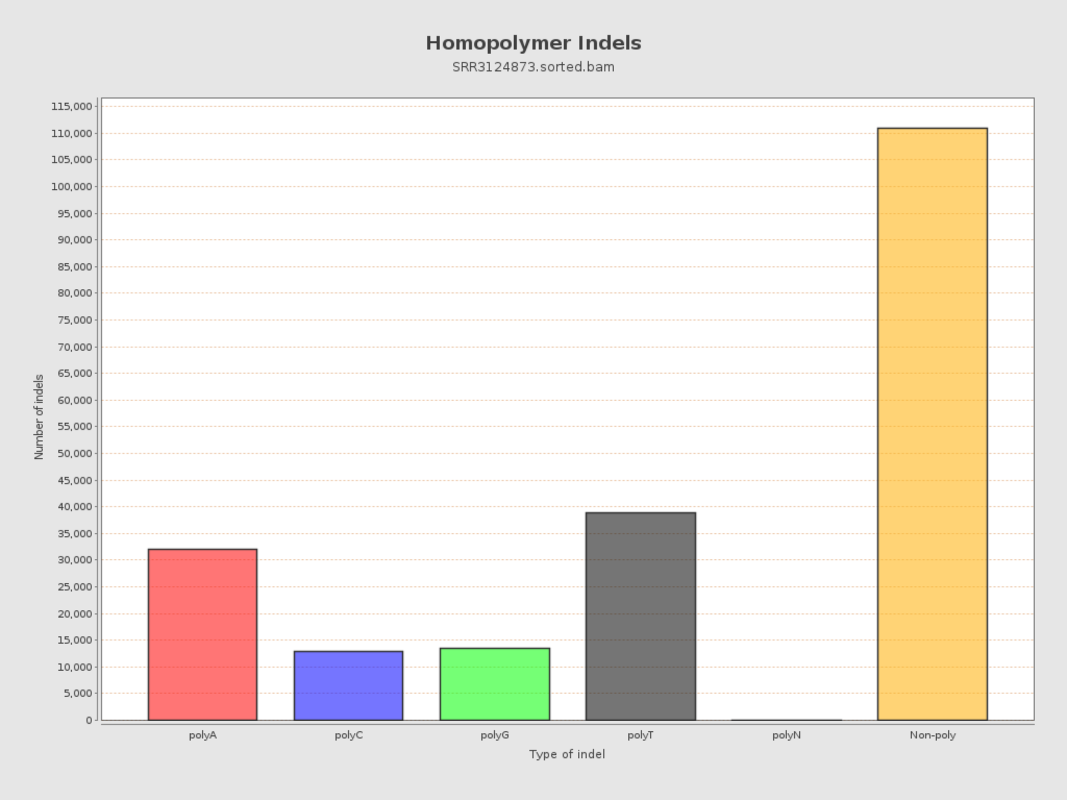
9. Results : Mapped Reads GC-content Distribution



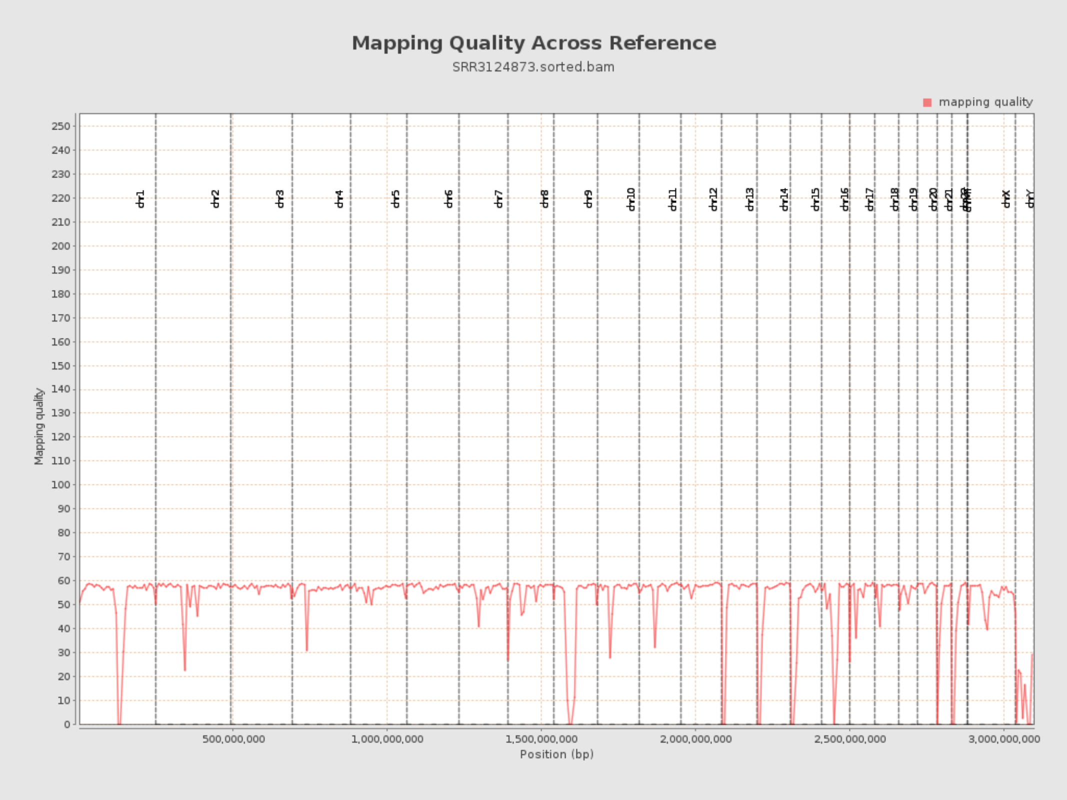
10. Results : Mapped Reads Clipping Profile



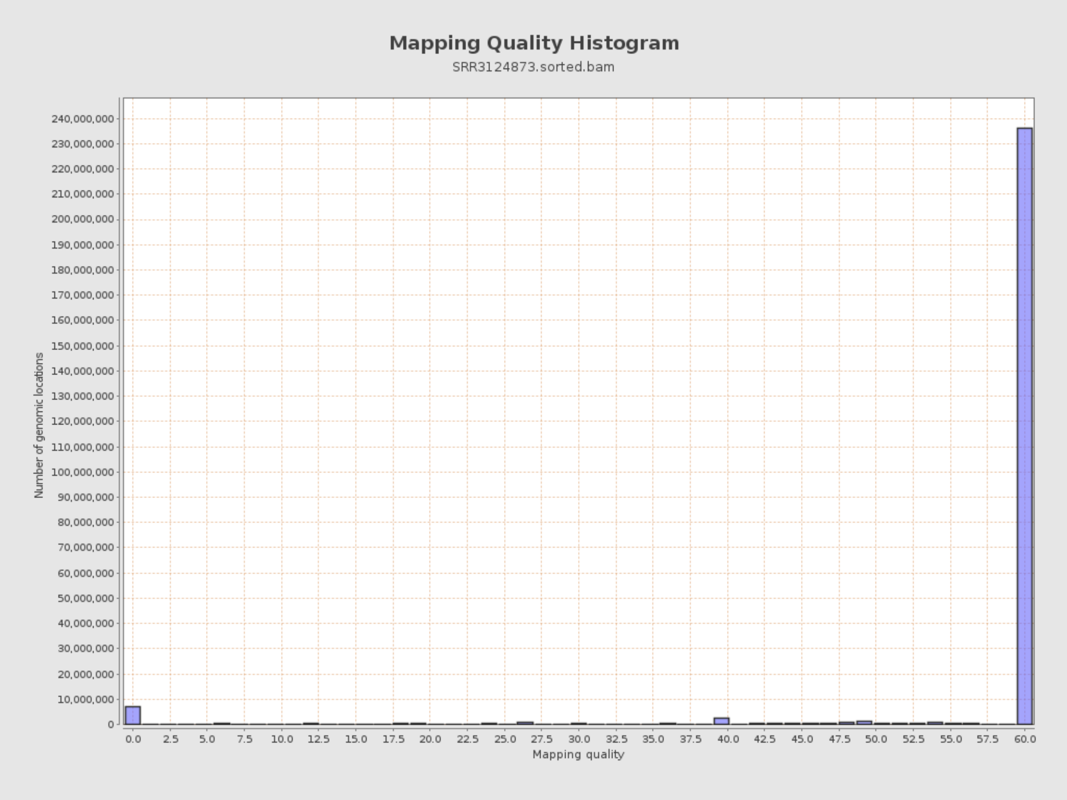
11. Results : Homopolymer Indels



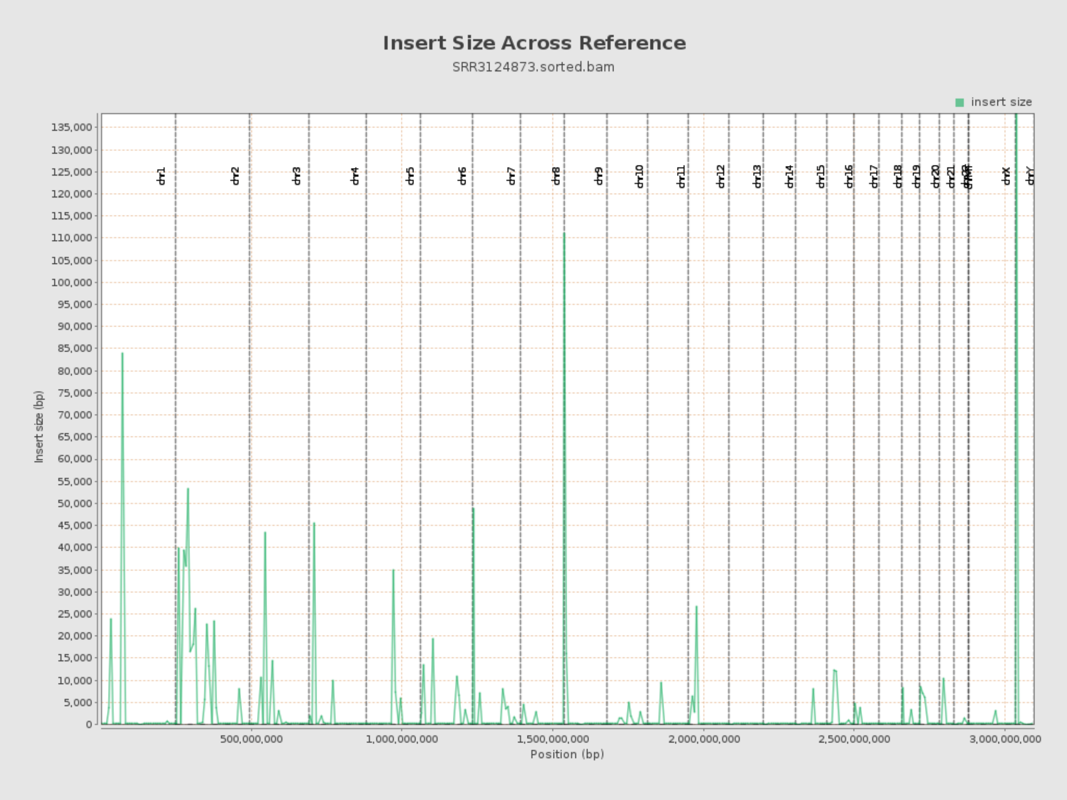
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram